

## CLAIMS

1. Chimeric promoter of gene expression comprising at least one transcriptional regulatory sequence from a gene encoding a high molecular weight wheat glutenin.

2. The chimeric promoter according to claim 1, wherein said at least one transcriptional regulatory sequence comprises a minimal promoter sequence from said gene encoding a high molecular weight glutenin which functions to activate transcription of a transcription unit operably linked to said chimeric promoter.

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3. Chimeric promoter according to Claim 1, wherein said gene encoding a high molecular weight wheat glutenin is the wheat Dx5 or Bx7 gene.

4. Chimeric promoter according to Claim 1, wherein said chimeric promoter comprises SEQ ID NO. 1.

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5. Chimeric promoter according to Claim 1, wherein said chimeric promoter comprises a sequence selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 3, SEQ ID NO. 4, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 11, SEQ ID NO. 12, SEQ ID NO. 13, SEQ ID NO. 16, SEQ ID NO. 17, SEQ ID NO. 8, SEQ ID NO. 19, SEQ ID NO. 20, SEQ ID NO. 21, and SEQ ID NO. 22.

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6. Chimeric promoter of gene expression comprising at least one transcriptional regulatory sequence from a gene encoding a high molecular weight wheat glutenin, and which comprises a TATA box and a transcription start site (+1)

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7. The chimeric promoter according to claim 6, wherein said at least one transcriptional regulatory sequence comprises a minimal promoter sequence from said gene encoding a high molecular weight glutenin which functions to activate transcription of a transcription unit operably linked to said chimeric promoter.

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8. Chimeric promoter according to Claim 6, further comprising at least one enhancer box upstream of the TATA box and the transcription start site (+1).

9. The chimeric promoter according to claim 8, wherein said enhancer box is functionally linked to said at least one regulatory sequence to increase transcription from said transcription start site at least 1.5-fold relative to a chimeric promoter without said enhancer box

10. Chimeric promoter according to Claim 8, further comprising at least one G-like box upstream of said at least one enhancer box.

11. The chimeric promoter according to claim 10, wherein said G-like box is functionally linked to said TATA box and transcription start site to increase transcription from said transcription start site at least 1.5-fold relative to a chimeric promoter without said G-like box.

12. Chimeric promoter according to claim 8 , further comprising at least one P-like box upstream of said at least one enhancer box.

13. Chimeric promoter according to claim 12, wherein said P-like box confers expression in the endosperm on a transcription unit operably linked to said chimeric promoter.

14. Chimeric promoter according to claim 8, further comprising at least one GATA box upstream of said at least one enhancer box.

15. The chimeric promoter according to claim 14, wherein said GATA box confers light-regulatable expression on a transcription unit operably linked to said promoter.

16. Chimeric promoter according to claim 8 , further comprising at least one cereal box upstream of the enhancer box.

17. Chimeric promoter according to claim 16, wherein said cereal box confers seed-specific expression on a transcription unit operably linked to said promoter.

18. Chimeric promoter according to claim 8, comprising two cereal boxes upstream of said at least one enhancer box wherein no transcriptional regulatory sequences are between said cereal boxes.

19. The chimeric promoter according to claim 18, wherein said cereal boxes are contiguous.

20. Chimeric promoter according to claim 6, further comprising at least one box selected from the group consisting of an as1 box, an as2 box, an as1/as2 box, an as2/as1 box, and combinations thereof, upstream of the transcription start site.

21. The chimeric promoter according to claim 20, wherein said at least one box confers root-specific expression on a transcription unit operably linked to said chimeric promoter.

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22. The chimeric promoter according to claim 20, wherein said at least one box activates expression of a transcription unit operably linked to said chimeric promoter in photosynthetic tissues.

23. Chimeric promoter according to claim 20, wherein said at least one box is downstream of said at least one enhancer box.

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24. Chimeric promoter according to claim 7, further comprising a GC-rich box upstream of said at least one enhancer box.

25. Chimeric promoter according to claims 7, comprising two cereal boxes upstream of the enhancer box, said enhancer box being upstream of an as2/as1 box.

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26. Chimeric promoter according to claim 6, further comprising at least one element selected from the group consisting of an enhancer box, a G-like box, a P-like box, a GATA box, a cereal box, an as1 box, an as2 box, an as1/as2 box, an as2/as1 box, and combinations thereof, wherein said chimeric promoter also further comprises a GC-rich box.

27. The chimeric promoter according to claim 26, wherein said GC rich box is downstream of said transcription start site.

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28. The chimeric promoter according to claim 26 or 27, wherein said GC rich box is in reverse orientation relative to said transcription start site.

29. Chimeric promoter according to claim 7, comprising at least one sequence selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 3, SEQ ID NO. 4, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 11, SEQ

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ID NO. 12, SEQ ID NO. 13, SEQ ID NO. 16, SEQ ID NO. 17, SEQ ID NO. 18, SEQ ID NO. 19, SEQ ID NO. 20, SEQ ID NO. 21 and SEQ ID NO. 22.

30. Expression cassette comprising the chimeric promoter of claim 1 operably linked to a transcription unit encoding a polypeptide, wherein said transcription unit is operably linked to a  
5 transcription termination nucleic acid sequence.

31. Expression cassette according to claim 30, wherein said chimeric promoter comprises SEQ ID NO. 1.

32. Expression cassette according to claim 30, wherein said chimeric promoter comprises a sequence selected from the group consisting of the numbers SEQ ID NO. 2, SEQ ID NO. 3, SEQ  
10 ID NO. 4, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 11, SEQ ID NO. 12, SEQ ID NO. 13, SEQ ID NO. 16, SEQ ID NO. 17, SEQ ID NO. 18, SEQ ID NO. 19, SEQ ID NO. 20, SEQ ID NO. 21 and SEQ ID NO. 22.

33. Isolated promoter nucleic acid sequence comprising SEQ ID NO. 1.

34. Isolated promoter nucleic acid sequence, comprising a sequence selected from the group consisting of SEQ ID NO. 2, SEQ ID NO. 3, SEQ ID NO. 4, SEQ ID NO. 5, SEQ ID NO. 6, SEQ ID NO. 7, SEQ ID NO. 8, SEQ ID NO. 9, SEQ ID NO. 10, SEQ ID NO. 11, SEQ ID NO. 12, SEQ ID NO. 13, SEQ ID NO. 16, SEQ ID NO. 17, SEQ ID NO. 18, SEQ ID NO. 19, SEQ ID NO. 20, SEQ ID NO. 21 and SEQ ID NO. 22.

35. Vector comprising a chimeric promoter according to claim 1, 5, or 7.

20 36. Vector comprising a promoter sequence or a functional element thereof, according to claim 33 or 34 for initiating the transcription of a transcription unit operably linked to said promoter system, said transcription unit encoding a polypeptide

37. Vector selected from the group consisting of pMRT1207, pMRT1177, pMRT1178, pMRT1179, pMRT1180 and pMRT1181.

25 38. Transgenic plant which has stably integrated into its genome at least one chimeric promoter sequence according to any of claims 1, 5, or 7.

39. Transgenic plant which has stably integrated into its genome at least one promoter sequence according to claim 33 or 34.

40. Transgenic plant according to Claim 38, wherein said plant is a dicotyledonous species.

41. The transgenic plant according to claim 40, wherein said dicotyledonous species is a species selected from the group consisting of potato, tobacco, cotton, lettuce, tomato, melon, cucumber, pea, rapeseed, beetroot or sunflower.

42. The transgenic plant according to claim 38, wherein said plant is a monocotyledonous species.

43. The transgenic plant according to claim 42, wherein said monocotyledonous species is selected from the group consisting of wheat, barley, oat, rice or maize.

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44. Propagule of a transgenic plant according to claim 38.

45. Propagule of a transgenic plant according to claim 44, wherein said propagule is a seed.

46. Cell comprising a chimeric promoter sequence or functional element thereof according to any of claims 1, 5, or 7.

47. Cell comprising a promoter sequence according to claim 33 or 34.

48. Cell according to claim 46, wherein said cell is a plant cell.

49. Cell according to claim 47, wherein said cell is a plant cell.

50. Method for expressing a nucleic acid sequence encoding a polypeptide in a cell, said method comprising the steps of:

transforming the cell with a vector according to claim 35; and

preparing a culture of the transformed cell under conditions which allow the expression of the nucleic acid sequence.

51. Method for expressing a nucleic acid sequence encoding a polypeptide in a cell, said method comprising the steps of:

transforming the cell with a vector according to claim 36;

5 preparing a culture of the transformed cell under conditions which allow the expression of the nucleic acid sequence.

52. Method according to claim 49 or 50, wherein said cell is a prokaryotic cell.

53. Method according to claim 49 or 50, wherein said cell is a eukaryotic cell.

54. Method according to claim 49 or 50, wherein said cell is selected from the group consisting of microbial cells, fungal cells, insect cells, animal cells and plant cells.

55. Method according to claims 49 or 50 wherein said cell is a plant cell.

56. Method according to claim 48 or 50, further comprising the step of isolating said polypeptide encoded by said nucleic acid sequence.

57. Method for obtaining a cell according to claim 46 comprising the steps of:

transforming a cell with a vector according to claim 35

15 selecting a cell which has integrated said chimeric promoter sequence into its genome; and

propagating the transformed and selected cell.

58. The method according to claim 56, wherein said cell is a plant cell.

59. The method according to claim 57, wherein said cell is a propagule.

20 60. The method according to claim 56, wherein said propagating is performed by culturing said cell.

61. The method according to claim 57, wherein said propagating is performed by regenerating chimeric or transgenic whole plants.